

FIG. 1.

Multiple Alignment:

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Sequence ID	Start Position	End Position	Sequence	Notes
30664188.099	1	100	MHR LI FVYTLLICANFC SCDTSATPQSASIKALRNAMLERIDESNHITDLYERRETIQWKG	60
VEGF-E	1	100	-MSLEFGLLIT SALAGQRQGTQAESNLSSK FQFSSNKK -EQNGVQDPQ -HERI ITWST	54
30664188.099	61	119	NGY PQS PRFPN SIFRNL LLT WRLHS -QENTRIQLWEDNQFGL EAENDICR YDFV EW EDI	119
VEGF-E	55	119	NGS IHS PRFPHIFTWRLWATVTEENWVQLTDERFGLDEDICK YDFV EVE EEP	114
30664188.099	120	179	SET ETI IRERWCGHKKEVPPRNIKERTTNQI KIT FKSDDYFVAKP3FKIIVYSLLED FQPA AAS	179
VEGF-E	115	179	SDG - TILERWCGSGT VFGK QIS KGNGQIRI REVSDEYFPSEPGFCIHYNL KMP - - - - - 165	165
30664188.099	180	238	ETNWVESVTSSISGGWSYNSPSVTDFTLIAADALDKKIAEFDWEDLIKWFNP E SWQEDLEN	238
VEGF-E	166	238	- - - QFTEAVS - - - - - PSVLP P3ALPLDLNNNAI TAESTEDLIKWL PERWQLDIED	214
30664188.099	239	296	WYL DTPRYR3FSYHD - RKS - KWIDLDRINDA KRVSCTPRNWSVNIREELK LANVVF FRC	296
VEGF-E	215	296	LYR PTWQQLLGEKA FVGRKSEVVDLNLTTEEVRLYSCTPRNWSVSIREELK RTDTTFWPGC	274
30664188.099	297	356	LLV QRC GGMCGEGTVMWR S CT CNSGKTVKKYHEVWLQFEPGHIKRRGRAKTMA IYD IQQLDH	356
VEGF-E	275	356	LLV KRC GGMCA CLHMNCNECQCVPSKVTKKYHEVQLRP - - KTGVR LLHK S LT DVA LEH	331
30664188.099	357	370	HERCDC13SSRPPR (SEQ ID NO:2)	370
VEGF-E	332	370	HECDC13VGRGSTGG (SEQ ID NO:28)	345

FIG. 2.

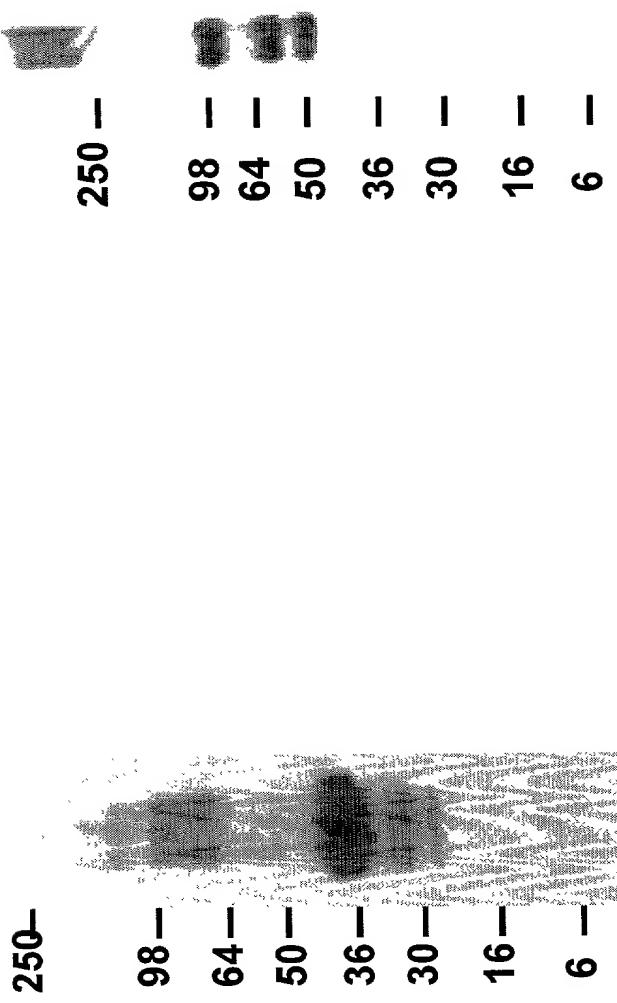
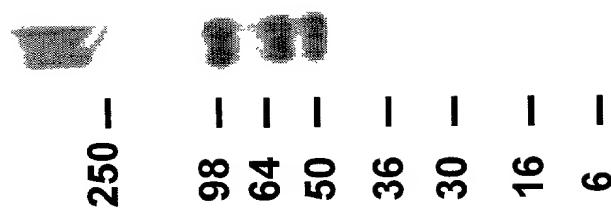


FIG. 3.

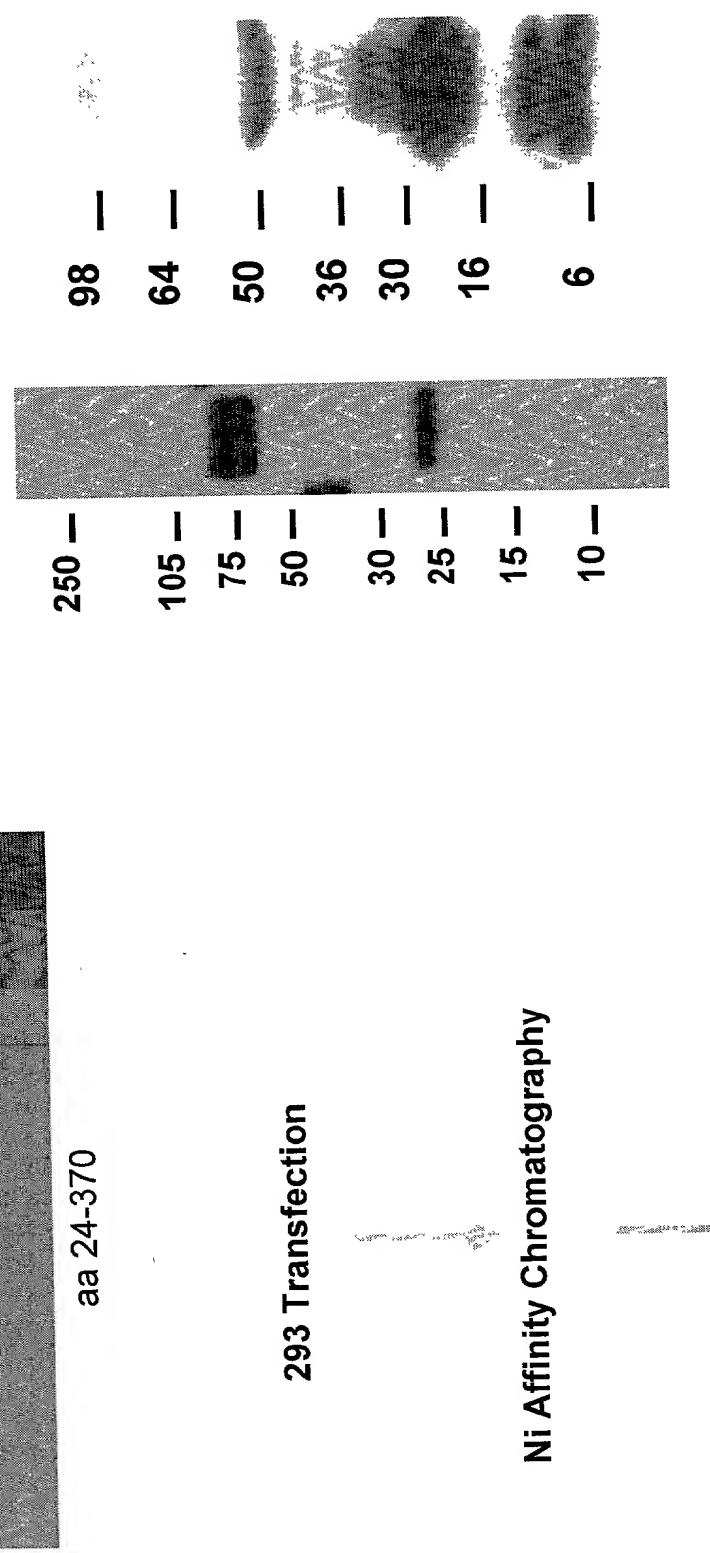


**FIG. 4A**

IgK      30664188      V5    His  
aa 24-370



**FIG. 4B**



Imidazole Elution

Ni Affinity Chromatography

FIG. 5.

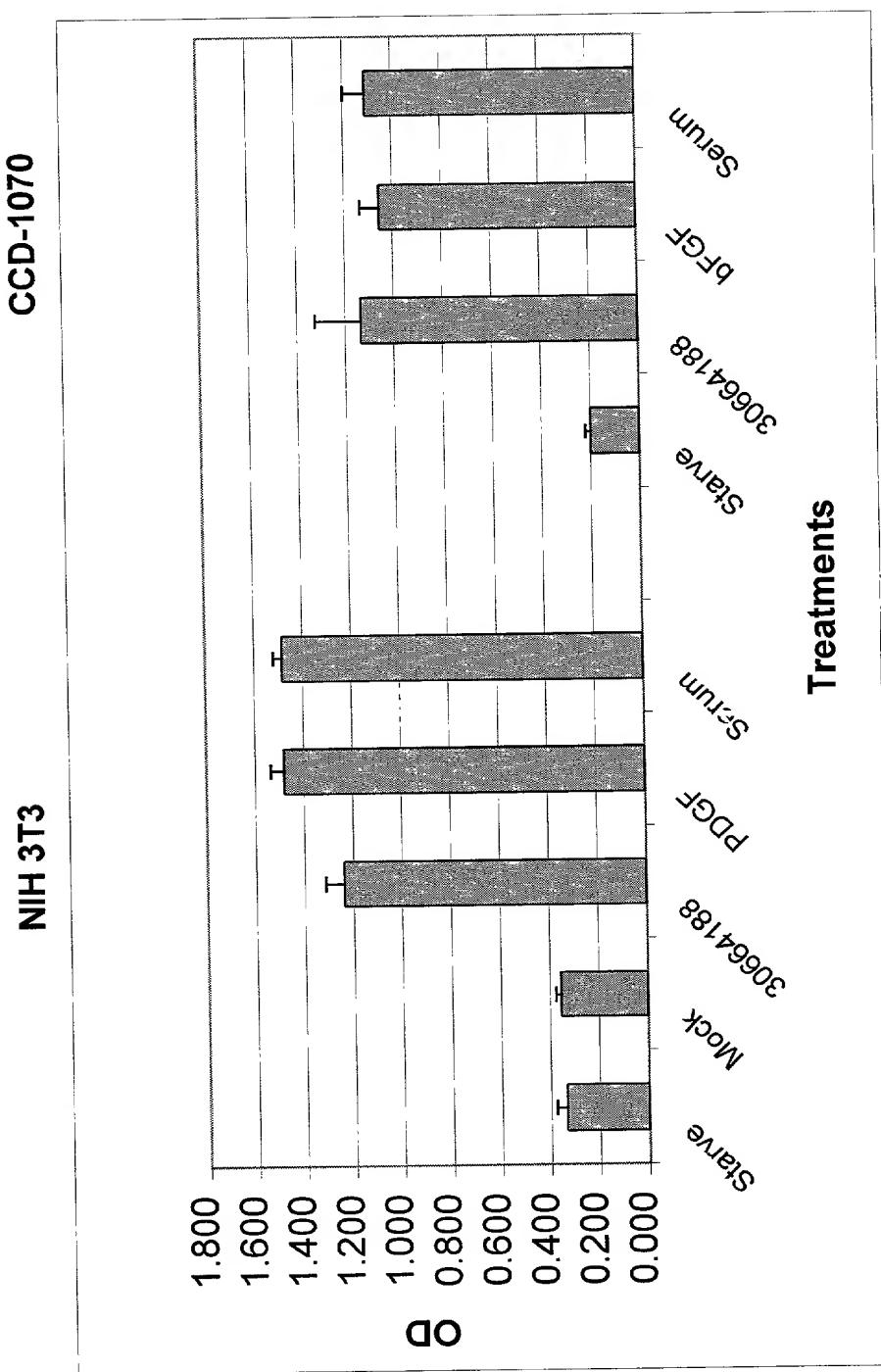


FIG. 6.

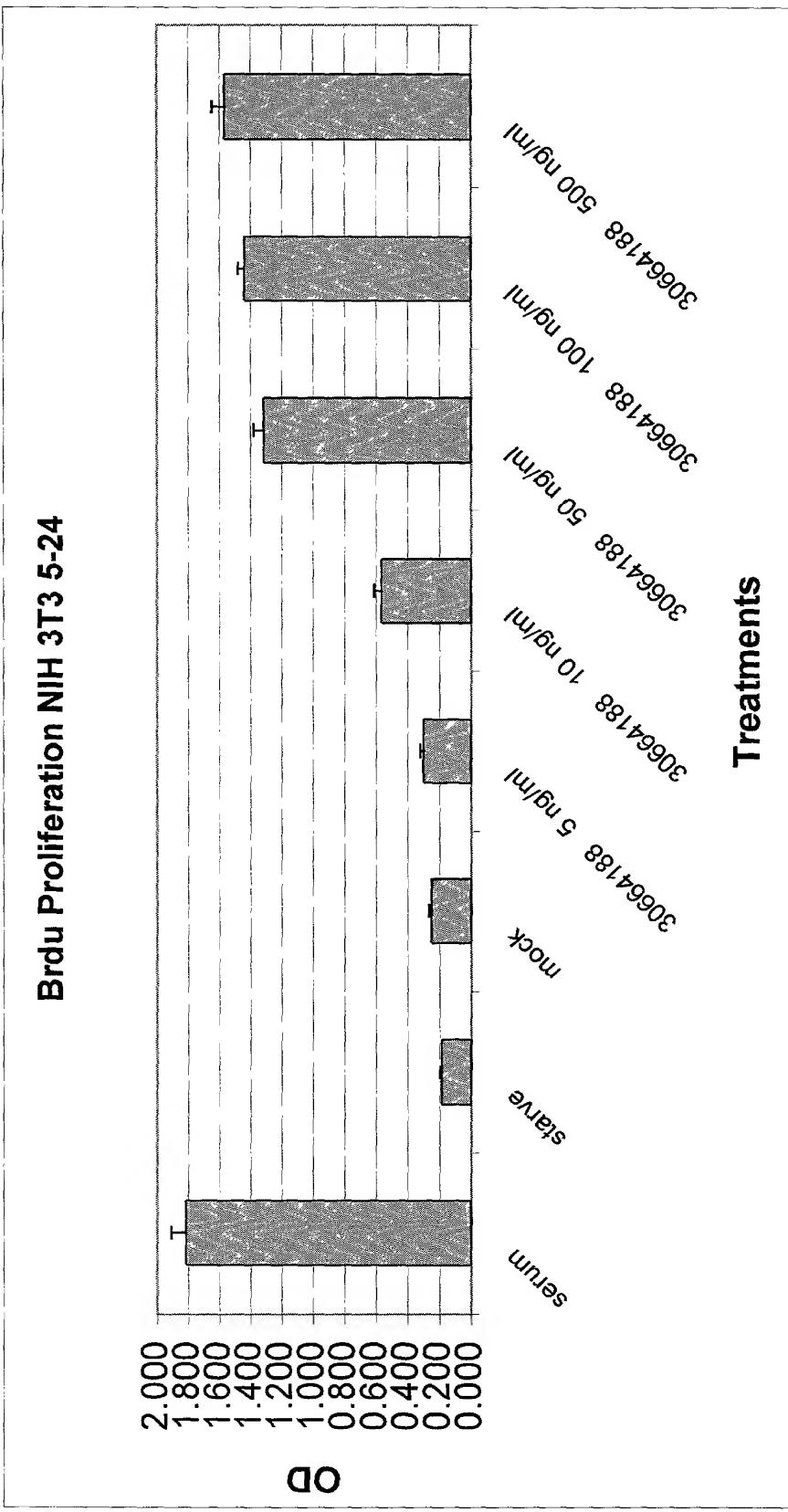


FIG. 7.

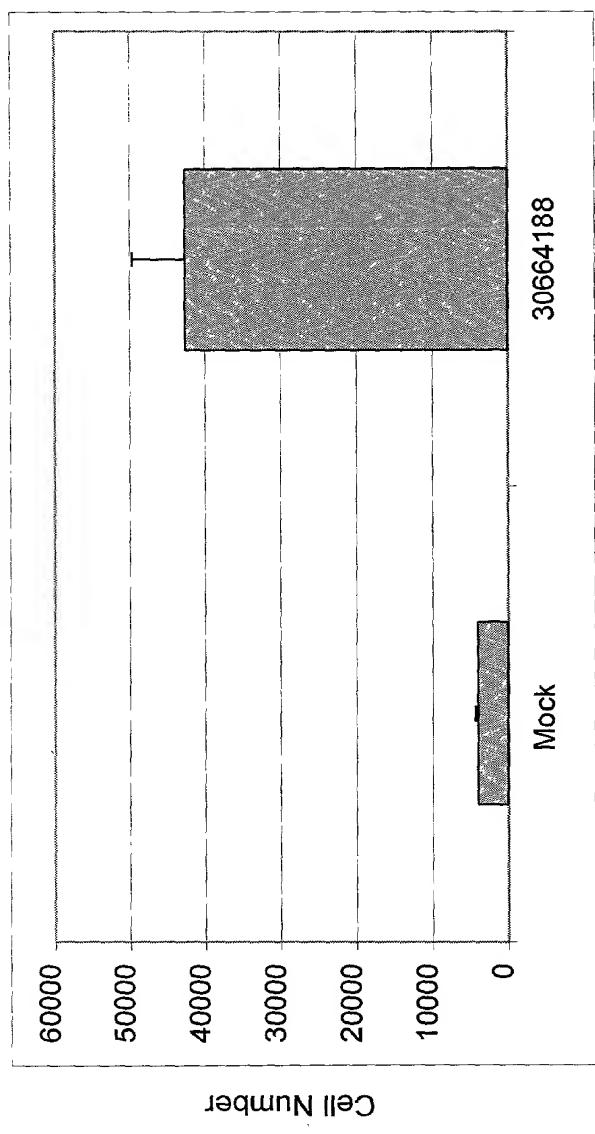


FIG. 8.

pCEP4sec(30664188) CM

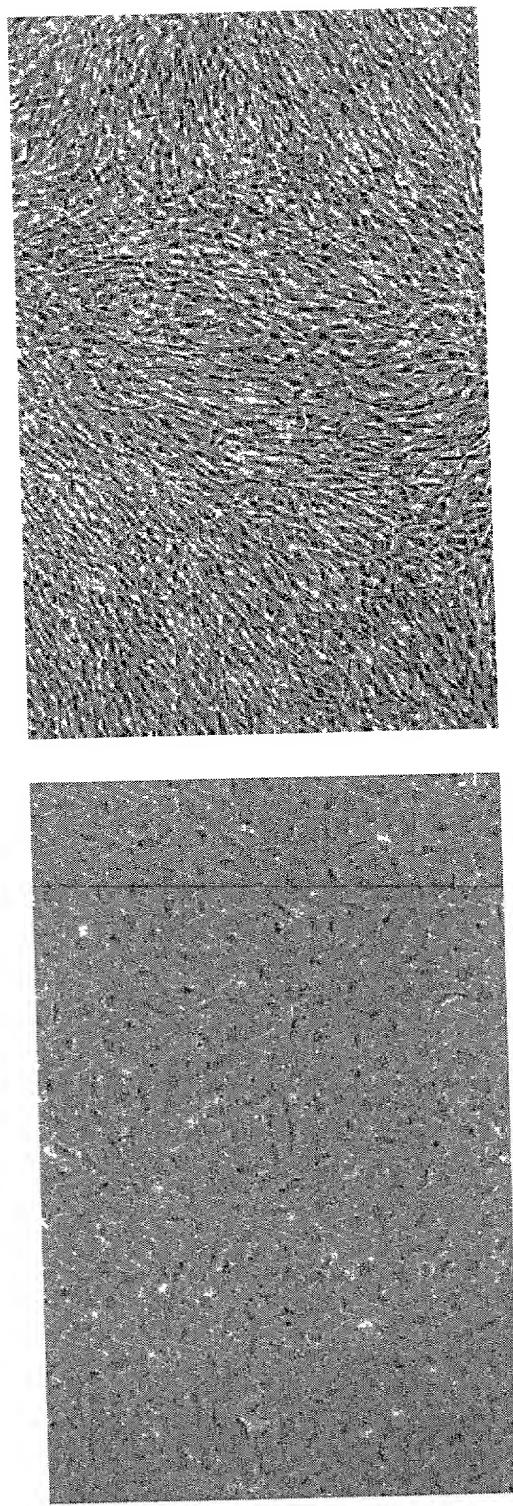


FIG. 9.

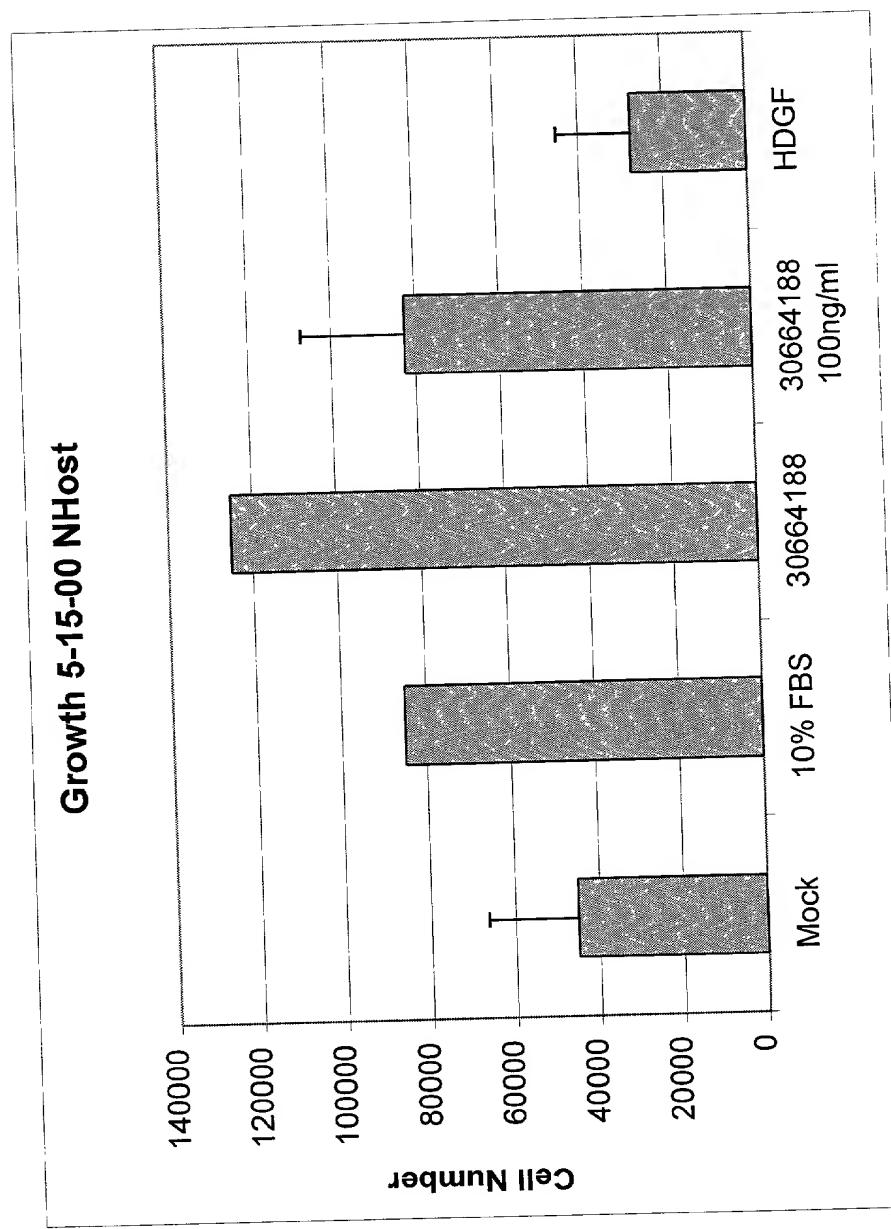


FIG. 10.

FIG. 10A (without serum)

Non-reducing  
Reducing  
M

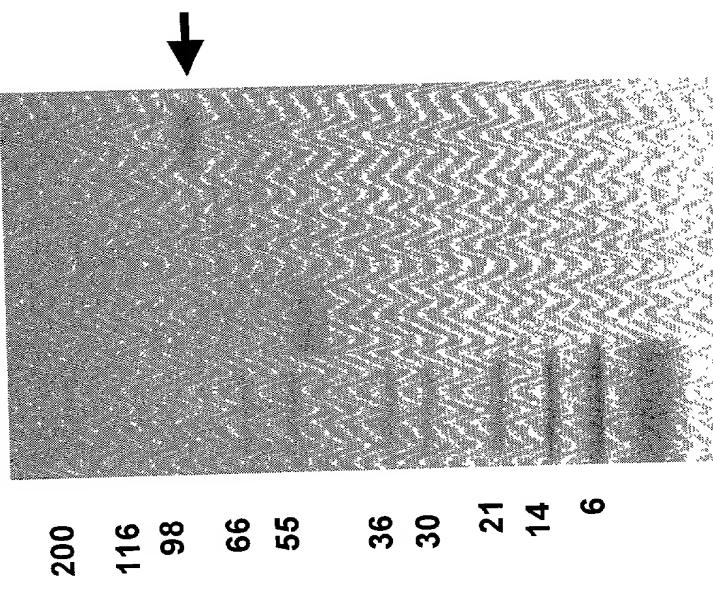


FIG. 10B (with serum)

Non-reducing  
Reducing  
M

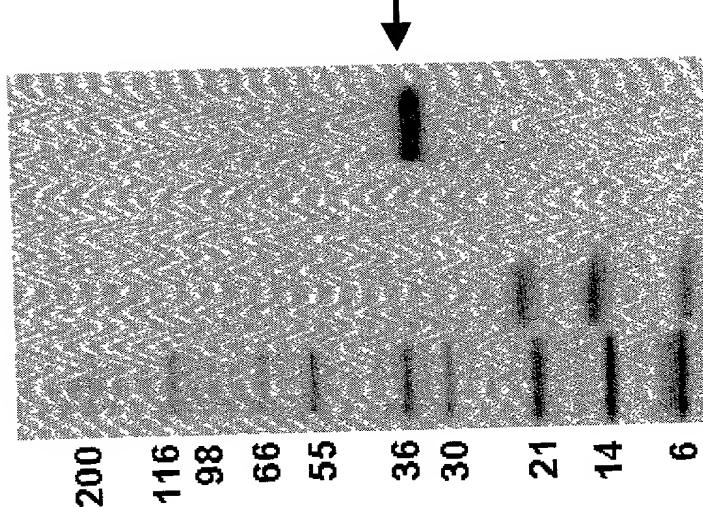


FIG. 11.

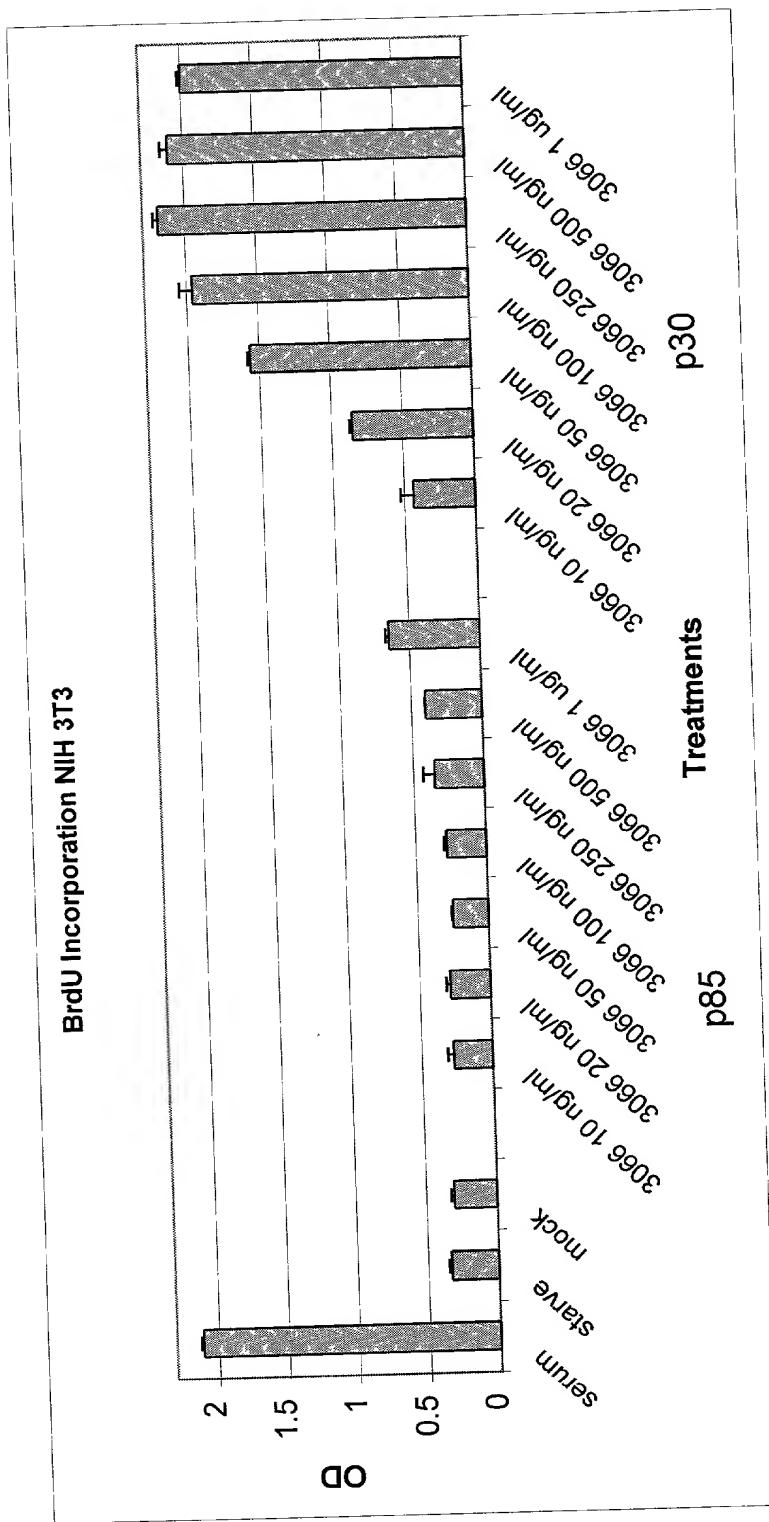


FIG. 12

\*  
hPDGF D CTPRNYSVNI-REELKLANVVF--FPRCLLVQRCGGNCGGTVNWRSCTC  
mPDGF D CTPRNHSVNL-REELKLTNAVF--FPRCLLVQRCGGNCGGTVNWKSCTC  
PDGF C CTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCGGNCACCLHNCNECQC  
PDGF B CKTRTEVFEISRRLIDRTNANFLVVPPCVEVQRCSG---CCNNRNVQCRP  
PDGF A CKTRTVIYEIPRSQVDPTSANFLIWPPCVEVKRCGTG---QCNNTSSVKCQP  
  
hPDGF D NS---GKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDC (SEQ ID NO:15)  
mPDGF D SS---GKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDC (SEQ ID NO:16)  
PDGF C VP---SKVTKKYHEVLQLRPKTGVRGLH-KSLTDVA--LEHHHECDC (SEQ ID NO:17)  
PDGF B TQVQLRPVQVRKIEIVRKKPIF----KKAT-VT----LEDHLACKC (SEQ ID NO:18)  
PDGF A SRVHHRSVKVAKVEYVRKKPKL----KEVQ-VR----LEEHLACAC (SEQ ID NO:19)

FIG. 13

Exon 1

1 CGCAGGGCGCCGGCGGTCCGTCGGCTCCGGAGCAGAACCCGGCTTTCTTGAGCGACGCTGTCTAGTCGCTGATCCCA

81 ATGCACCGGGCATCTTGTCTACACTCTAATCTGCCAAACTTTGCAGCTGTCGGACACTCTGCAACCCCCAGA  
M H R L I F V Y T L I C A N F C S C R D T S A T P Q S

161 GGCATCCATCAAAGCTTGCACGGCAACCTCAGCGAGATGAGAGCAATCACCTCACAGACTTGTACCGAAGAGAT  
A S I K A L R N A N L R R D E S N H L T D L Y R R D

241 GAGACCATCCAGGTGAAAGAACGGCTACGTGCAGAGTCCTAGATTCGGAACAGCTACCCCAGGAACCTGCTCTGAC  
E T I Q V K G N G Y V Q S P R F P N S Y P R N L L T

321 ATGGCGGCTTCACTCTCAGGAGAACACGGATAACAGTAGTGTGACAATCAGTTGGATTAGAGGAAGCAGAAAATG  
W R L H S Q E N T R I Q L V F D N Q F G L E E A E N D

401 ATATCTGTAGGTATGATTGTGGAAAGTGAAGATATATCGAAACCACTGACATTAGAGGACGATGGTGTGGACAC  
I C R Y D F V E V E D I S E T S T I I R G R W C G H

481 AAGGAAGTTCCTCCAAGGATAAAATCAAGAACGAAACCAATTAAATCACATTCAAGTCCGATGACTACTTTGGCTAA  
K E V P P R I K S R T N Q I K I T F K S D D Y F V A K

561 ACCTGGATTCAAGATTATTATTCTTCTGCGAAGATTCCAACCCGAGCAGCTCAGAGACCAACTGGGAATCTGTCA  
P G F K I Y Y S L L E D F Q P A A A S E T N W E S V T

641 CAAGCTCTATTCTAGGGTATCCTATAACTCTCCATCACTGAACTGGATCCACTCTGATTGCGGATGCTCTGGACAAAAAA  
S S I S G V S Y N S P S V T D P T L I A D A L D K K

721 ATTGCGAGAATTGATAACAGTGGAAAGATCTGCTCAAGTACTTCAACTCAGAGTCATGCCAAGAAGATCTTGAGAATATGTA  
I A E F D T V E D L L K Y F N P E S U Q E D L E N M Y

801 TCTGGACACCCCTCGGTATCGAGGCAGGTCAATCCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATG  
L D T P R Y R G R S Y H D R K S K V D L D R L N D D A

881 CCAAGCGTTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAGCTGAAGTTGGCCAATGTGGCTTCTCTT  
K R Y S C T P R N Y S V N I R E E L K L A N V V F F

961 CCACGTTGCCCTCTCGTCAGCGCTGTGGAGGAATTGTGGCTGTGAACTGTCAACTGGAGGTCTGCACATGCAATT  
P R C L L V Q R C G G N C G C G T V N W R S C T C N S

1041 AGGGAAAACCGTAAAAAGTATCATGAGGTATTACAGTTGAGCCTGGCACATCAAGAGGAGGGTAGAGCTAACGACCA  
G K T V K K Y H E V L Q F E P G H I K R R G R A K T M

1121 TGGCTCTAGTTGACATCCAGTTGGATCACCCTGAACGATGTGATTGTATCTGCAGCTCAAGACCAACCTCGATAAGAGAT  
A L V D I Q L D H H E R C D C I C S S R P P R (SEQ ID NO:20)

1201 GTGCACATCCTTACATTAAGCCTGAAAGAACCTTGTAGTTAAGGAGGGTAGAGATAAGAGACCCCTTCTACCAAGCAAC

1281 AAACTTACTACTAGCCTGCAATGCAATGAAACACAAGTGGTTGCTGAGTCAGCCTGCTTGTAAATGCCATGGCAAGT

1361 AGAAAGGTATATCATCAACTCTATACCTAAGAATATAGGATTGCATTAAATAATAGTGTGAGGTTATATATGCACAA

1441 ACACACACAGAAAATATTATCATGTCTATGTATATAGATCAAATGTTTTGGTATATATAACCAGGTACACCAGAG

1521 CTTACATATGTTGAGTTAGACTCTTAAATCCTTGGCAAAATAAGGGATGGTCAAATATATGAAACATGTCTTGTAGAA

1601 AATTAGGAGATAAAATTATTTAAATTGAAACACAAACAAATTGTGAATCTGCTCTTAAAGAAAGCATCTTGT  
Exon 7

1681 ATATTAATCAAAGATGAGGCTTCTACATATACATCTTAGTTC (SEQ ID NO:21)

FIG. 14

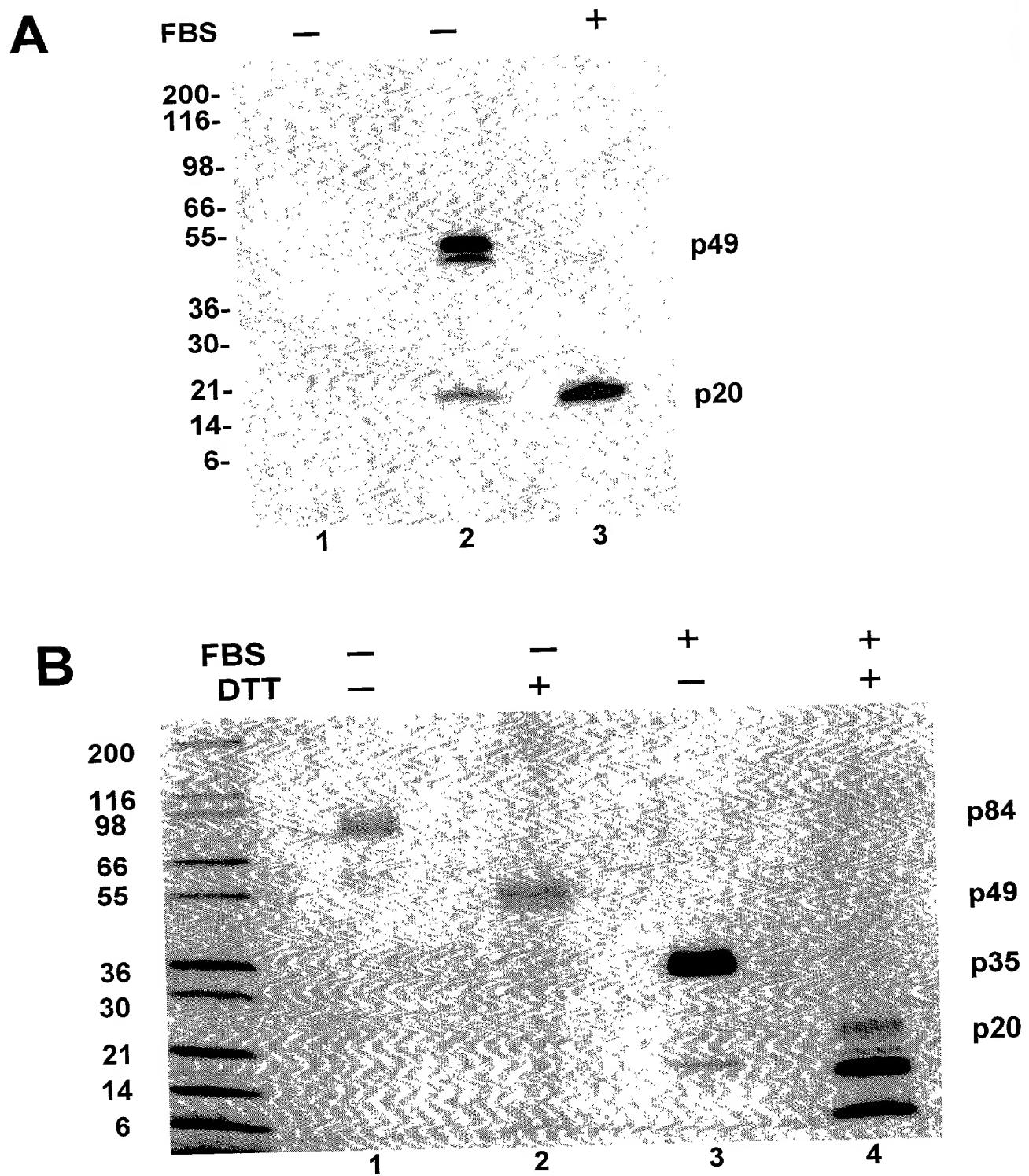


FIG. 15

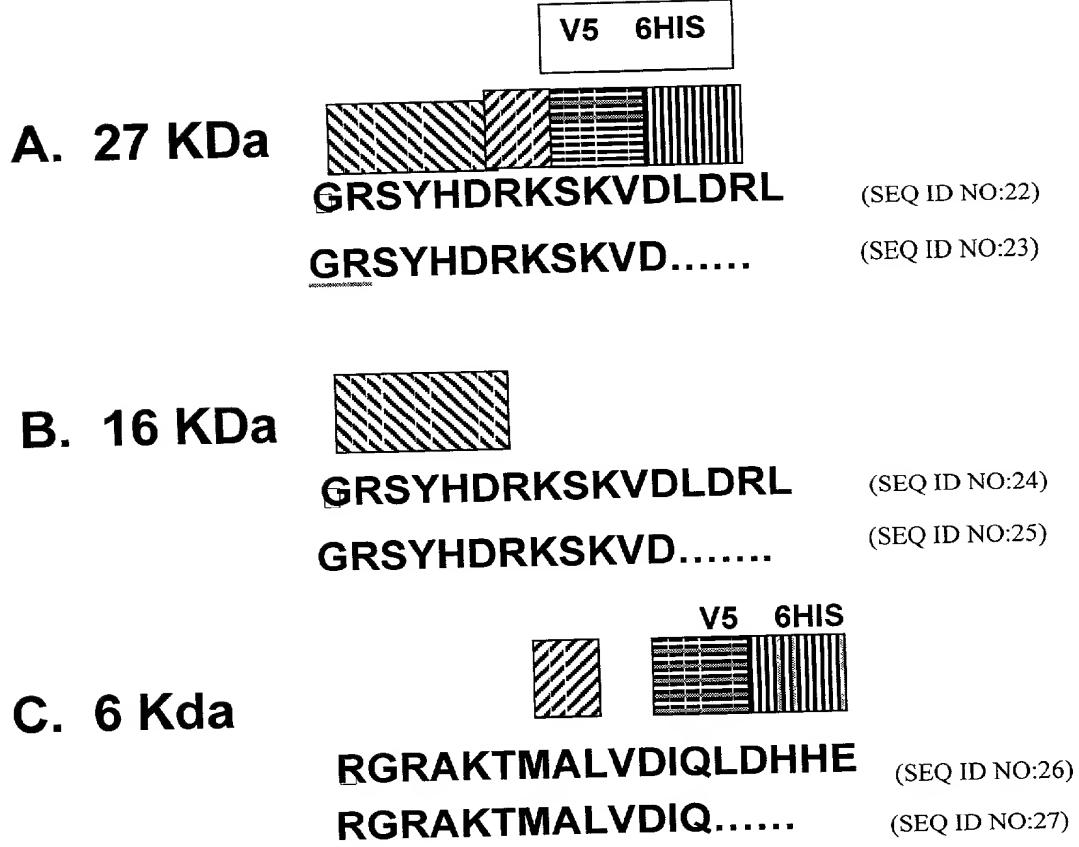


FIG. 16

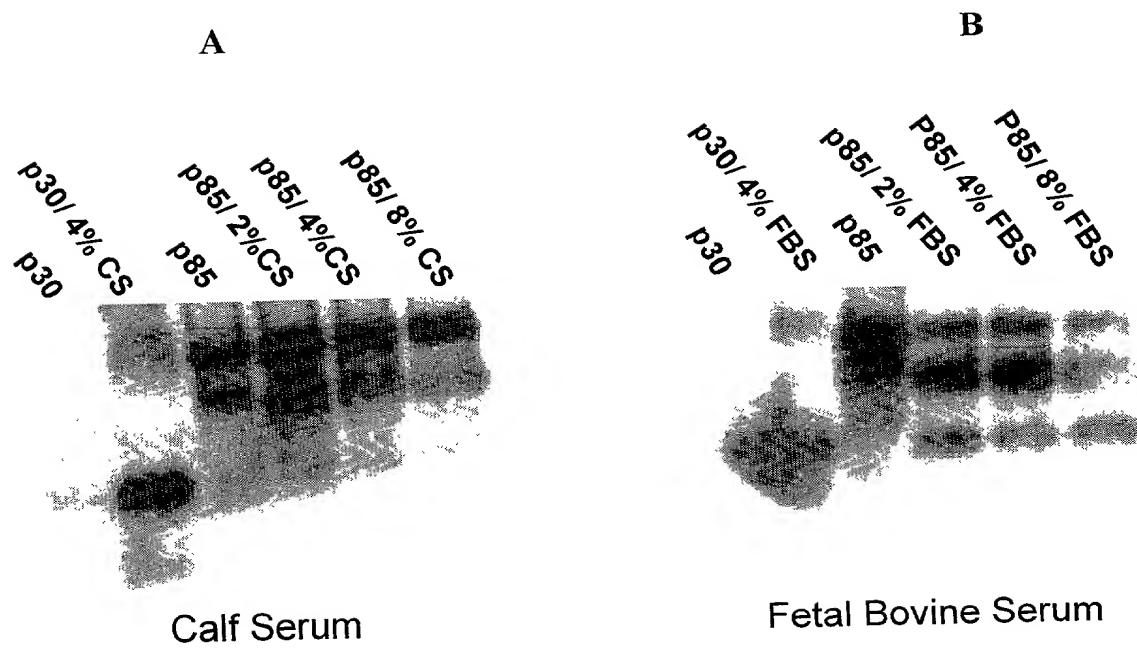


FIG. 17

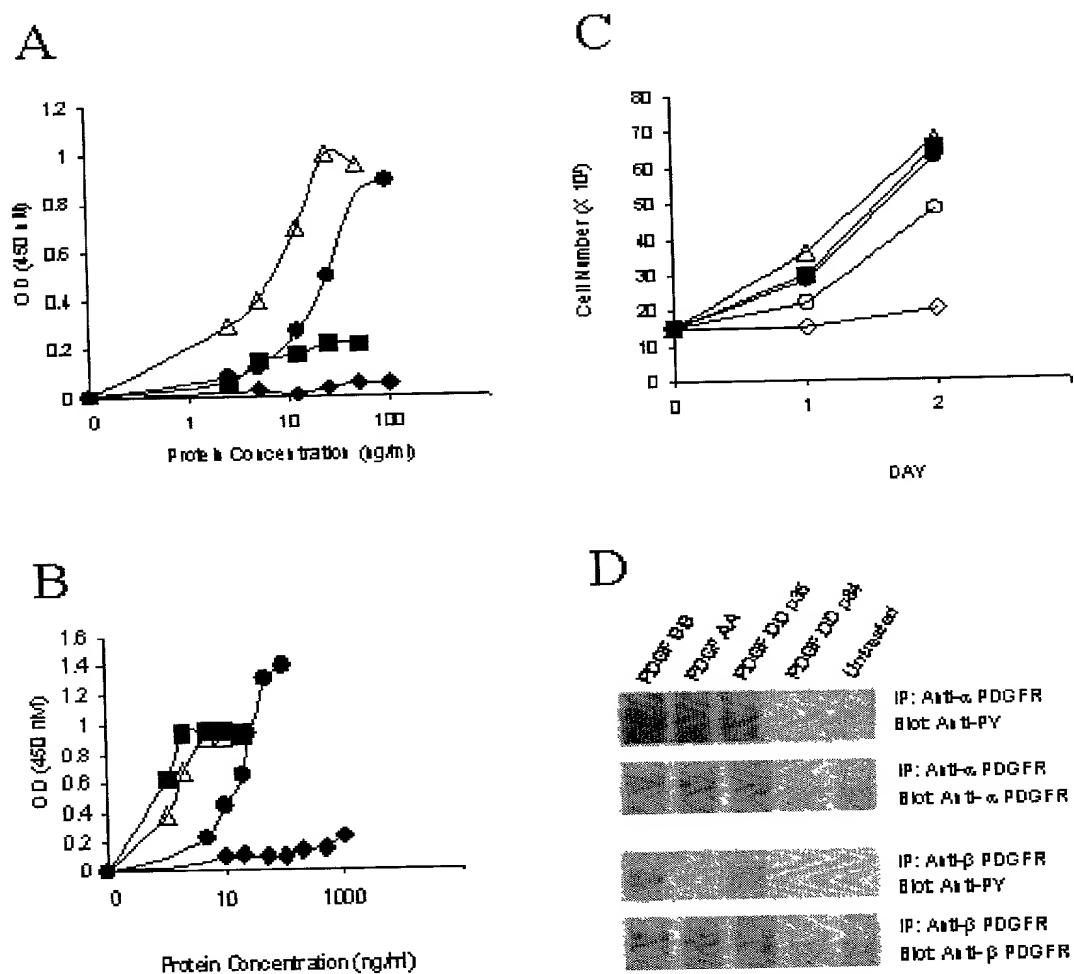


FIG. 18

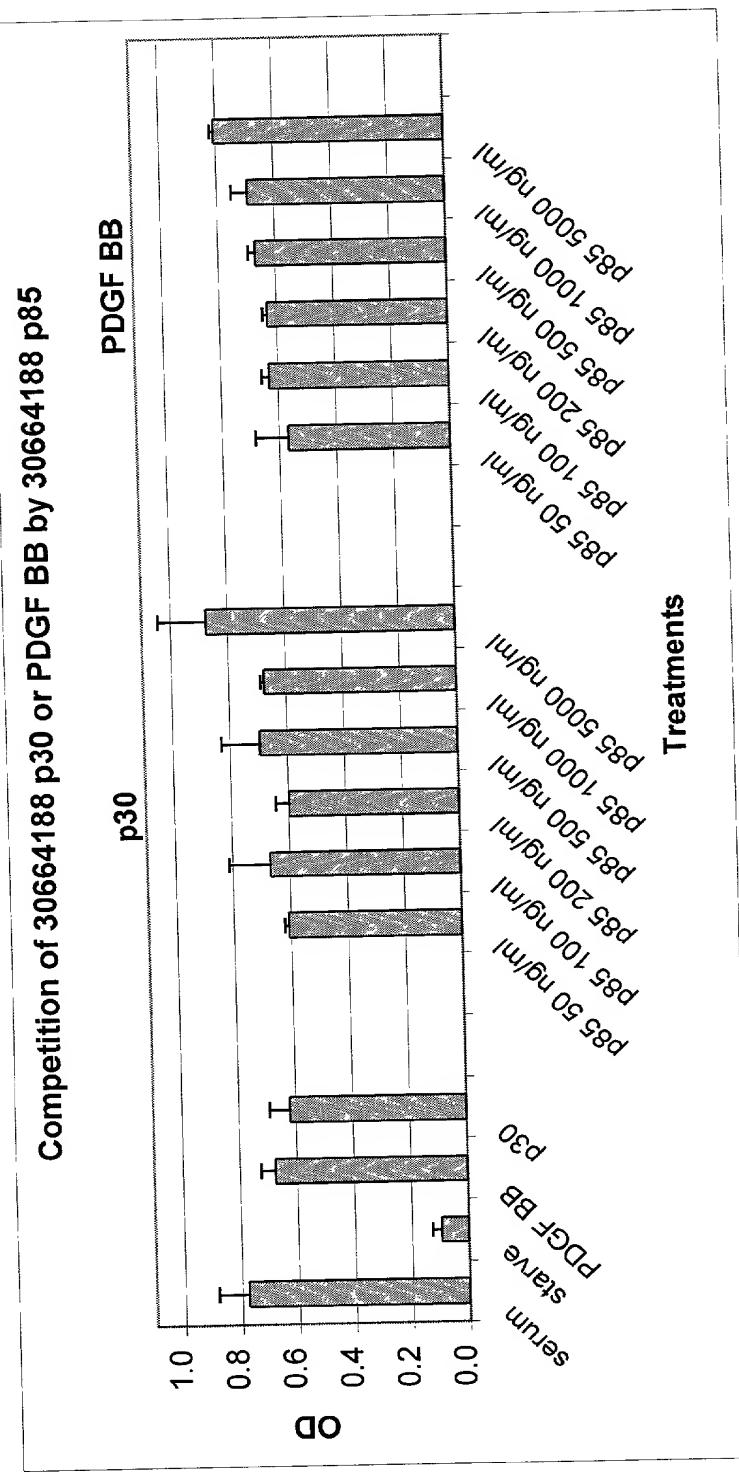


FIG. 19

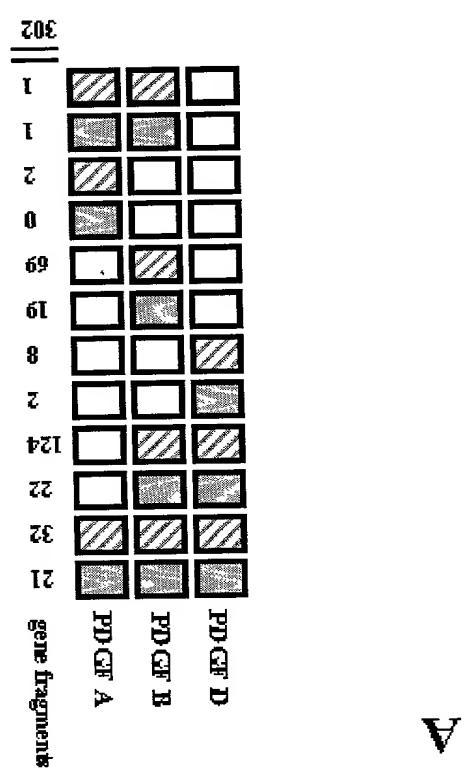


FIG. 20

CCD1070 Growth: Competition by Anti-Receptor Antibodies

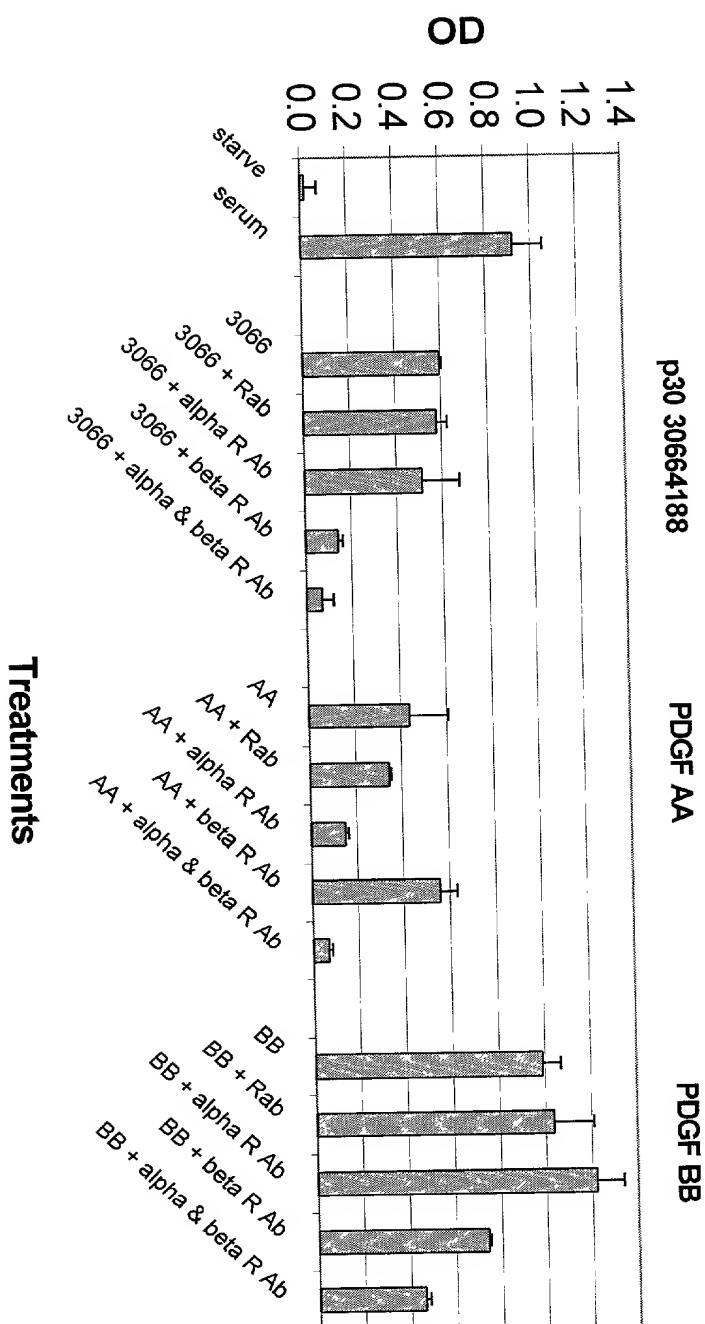


FIG. 21

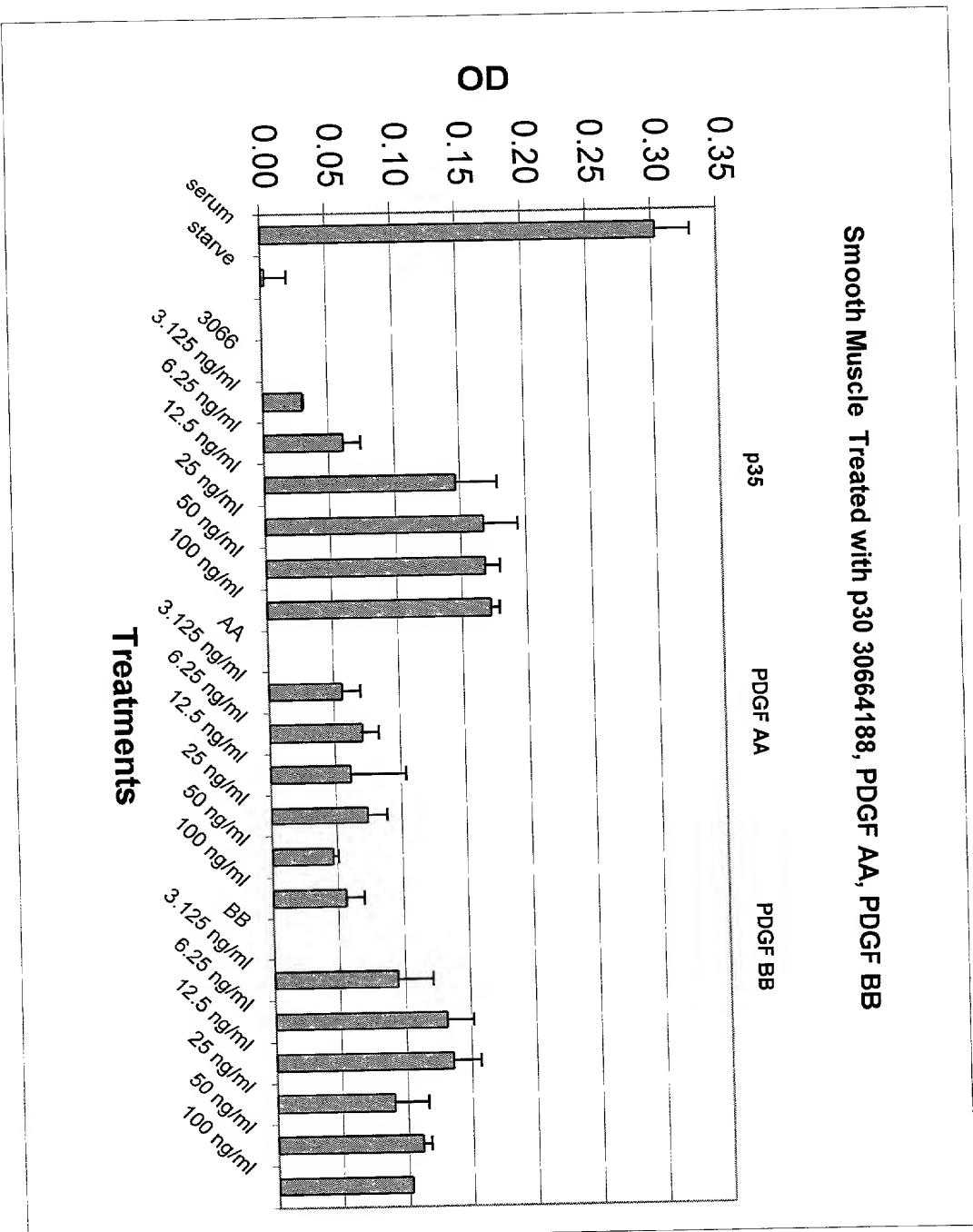


FIG. 22

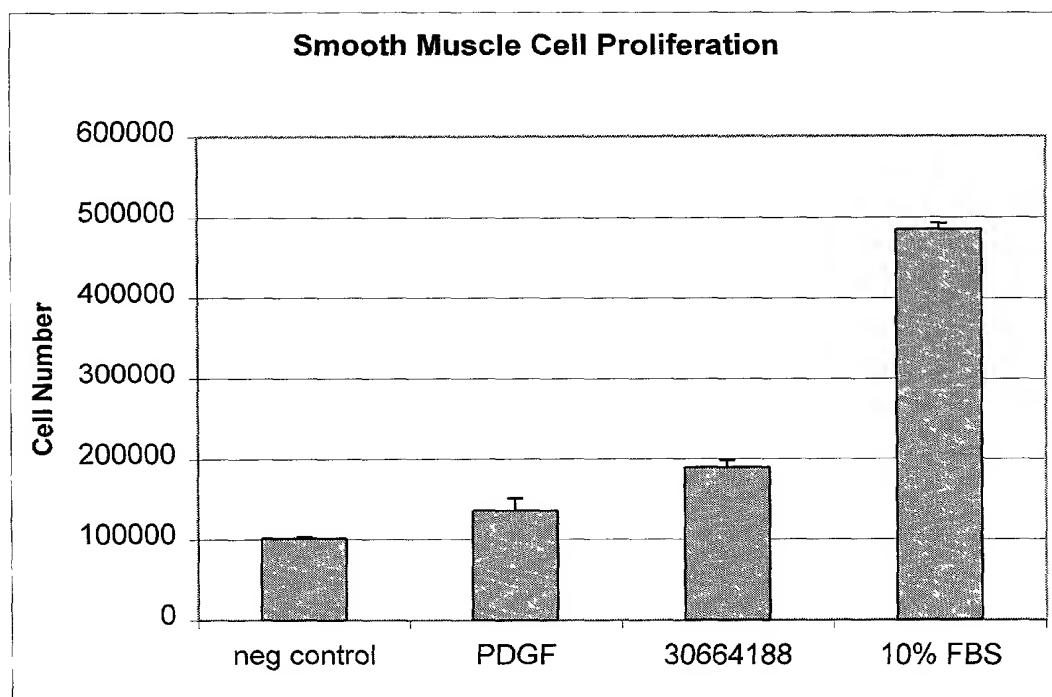


FIG. 23

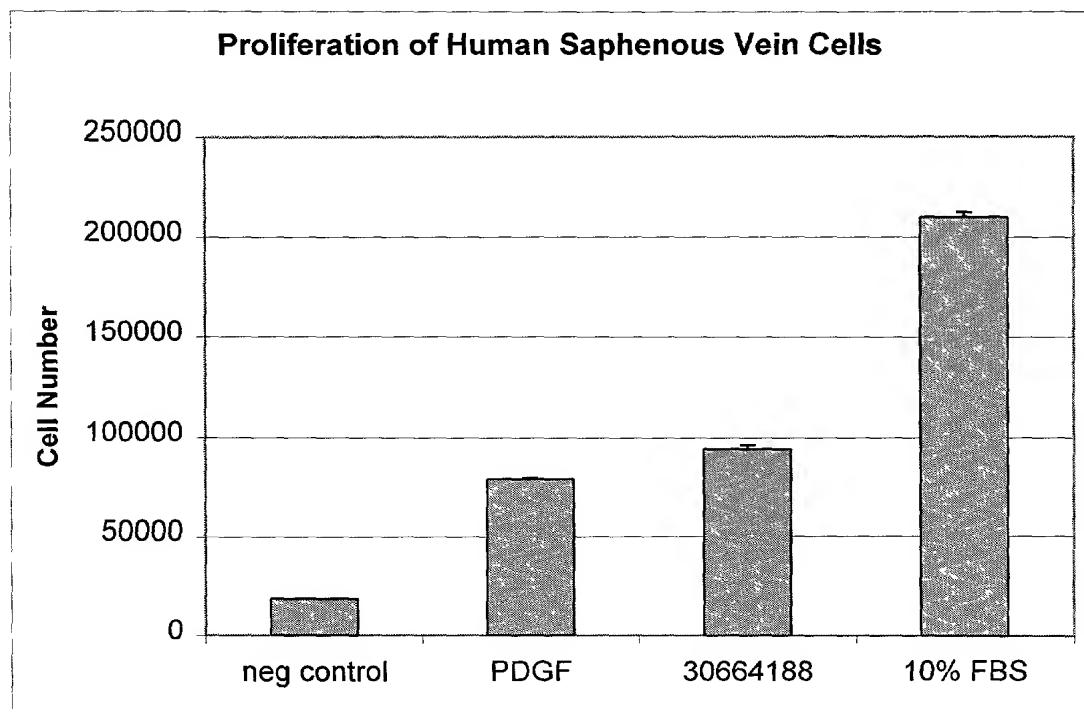
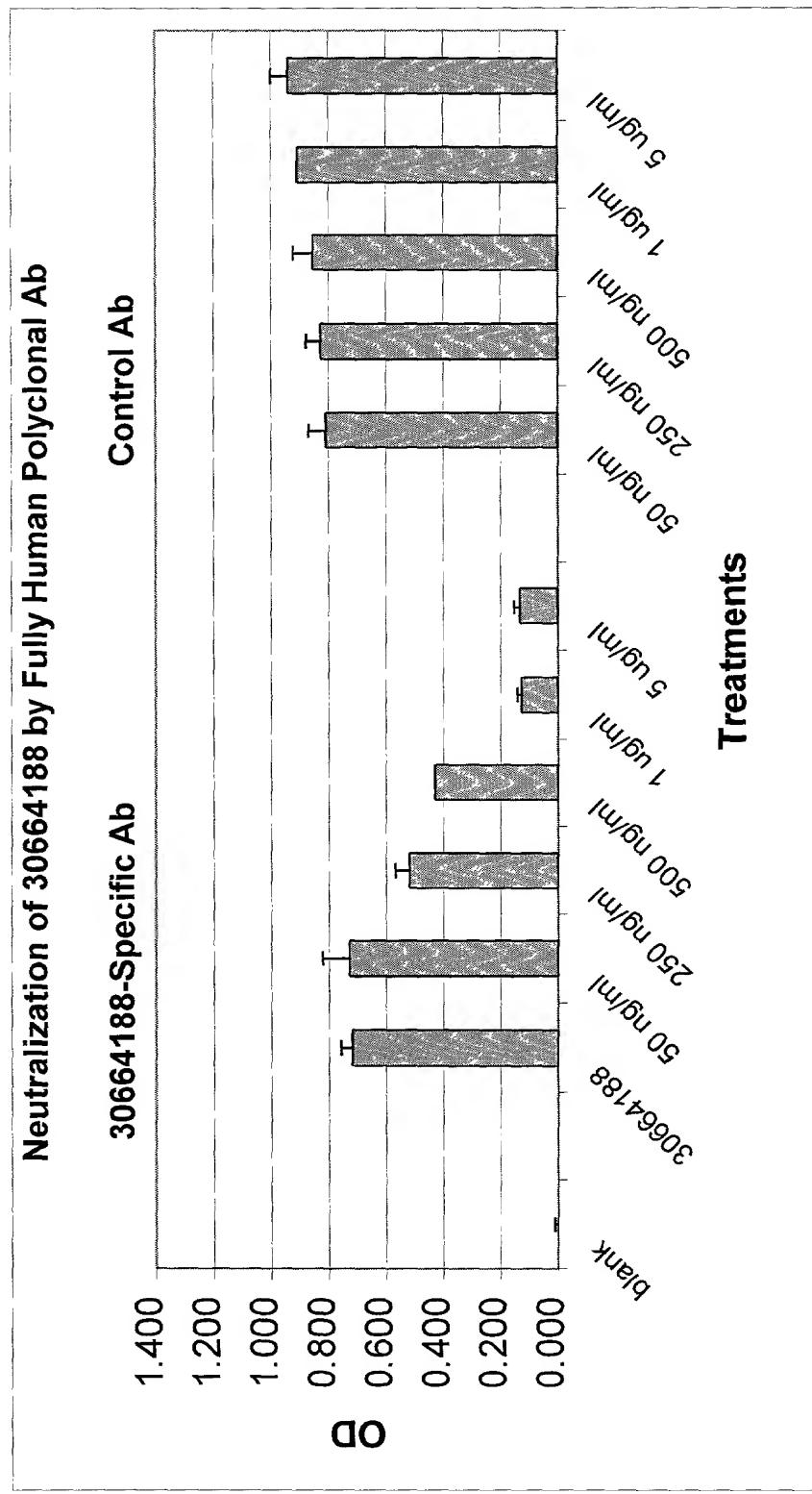
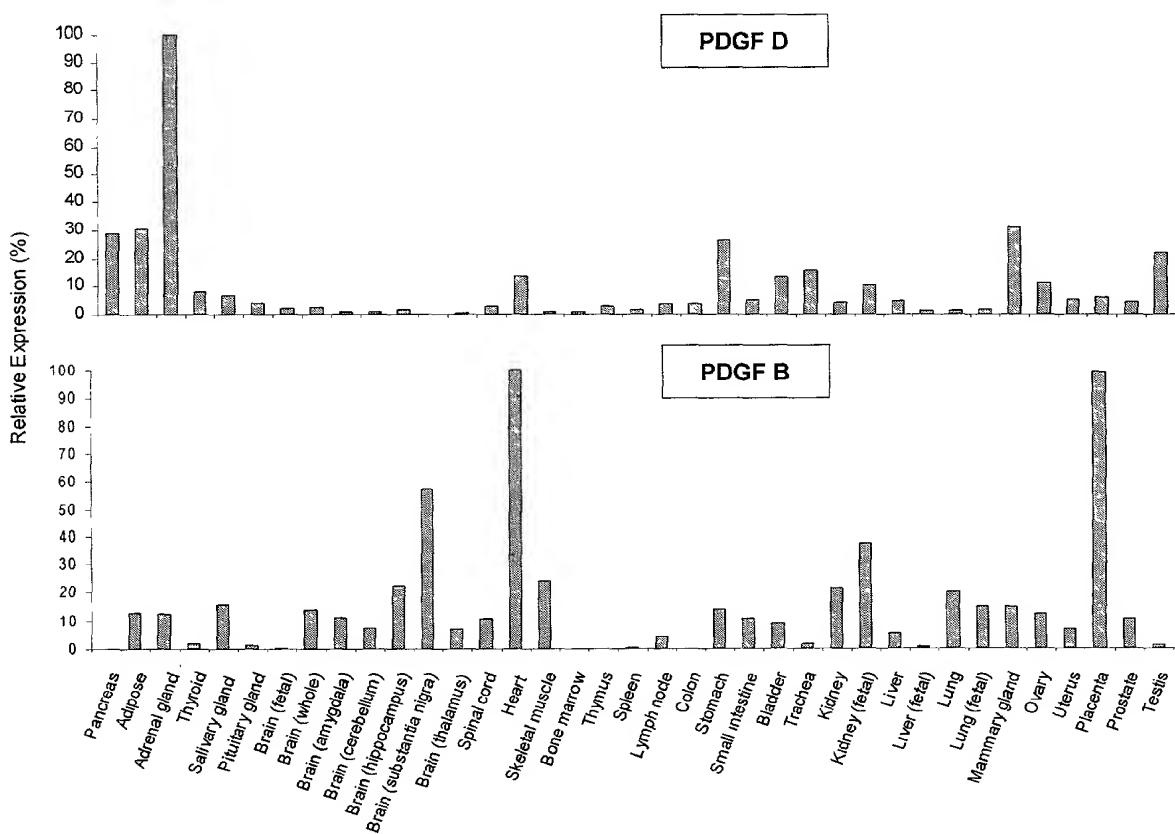


FIG. 24



**Fig. 25.**

**Panel A**



**Fig. 25 (cont.)**

**Panel B**

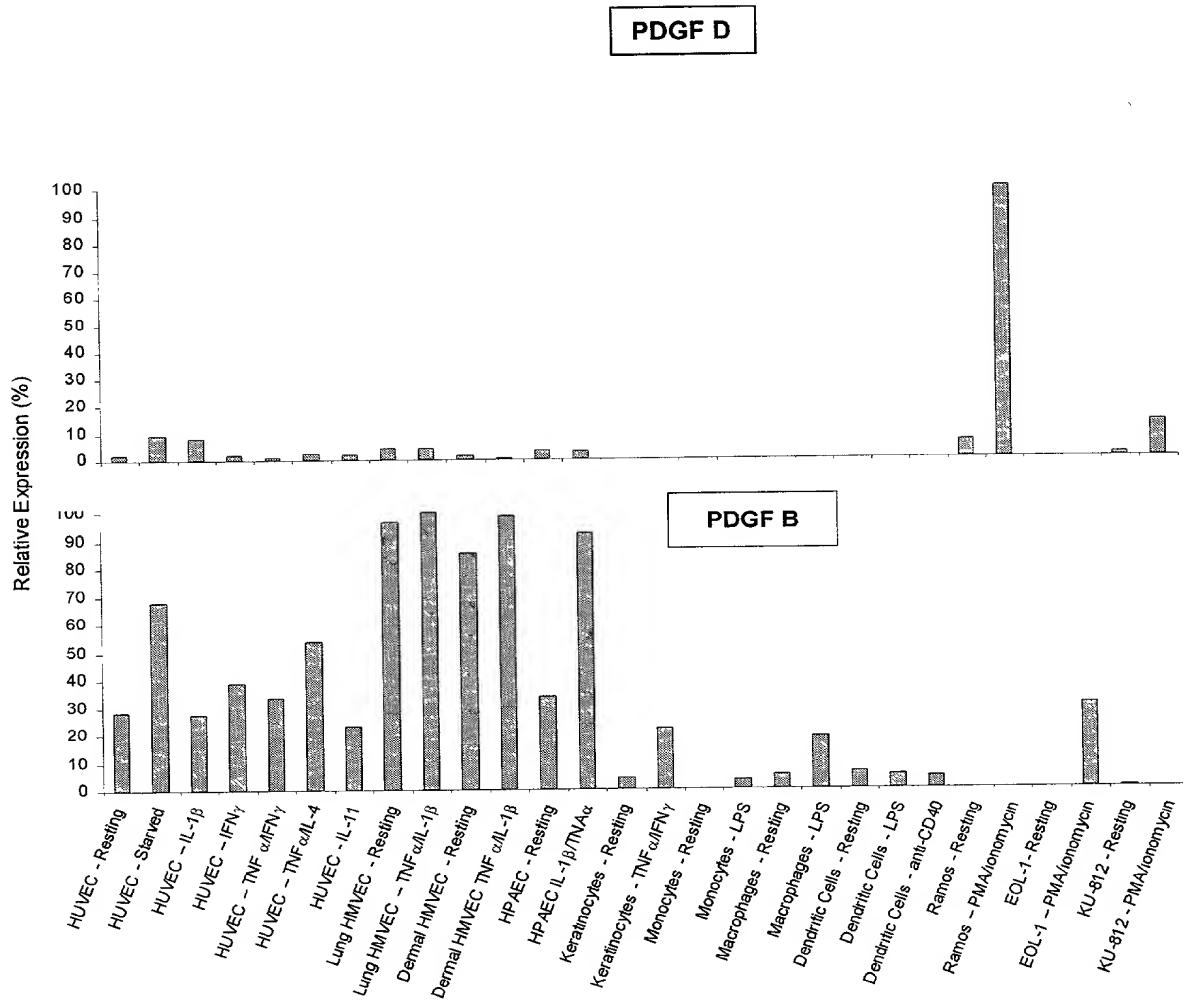
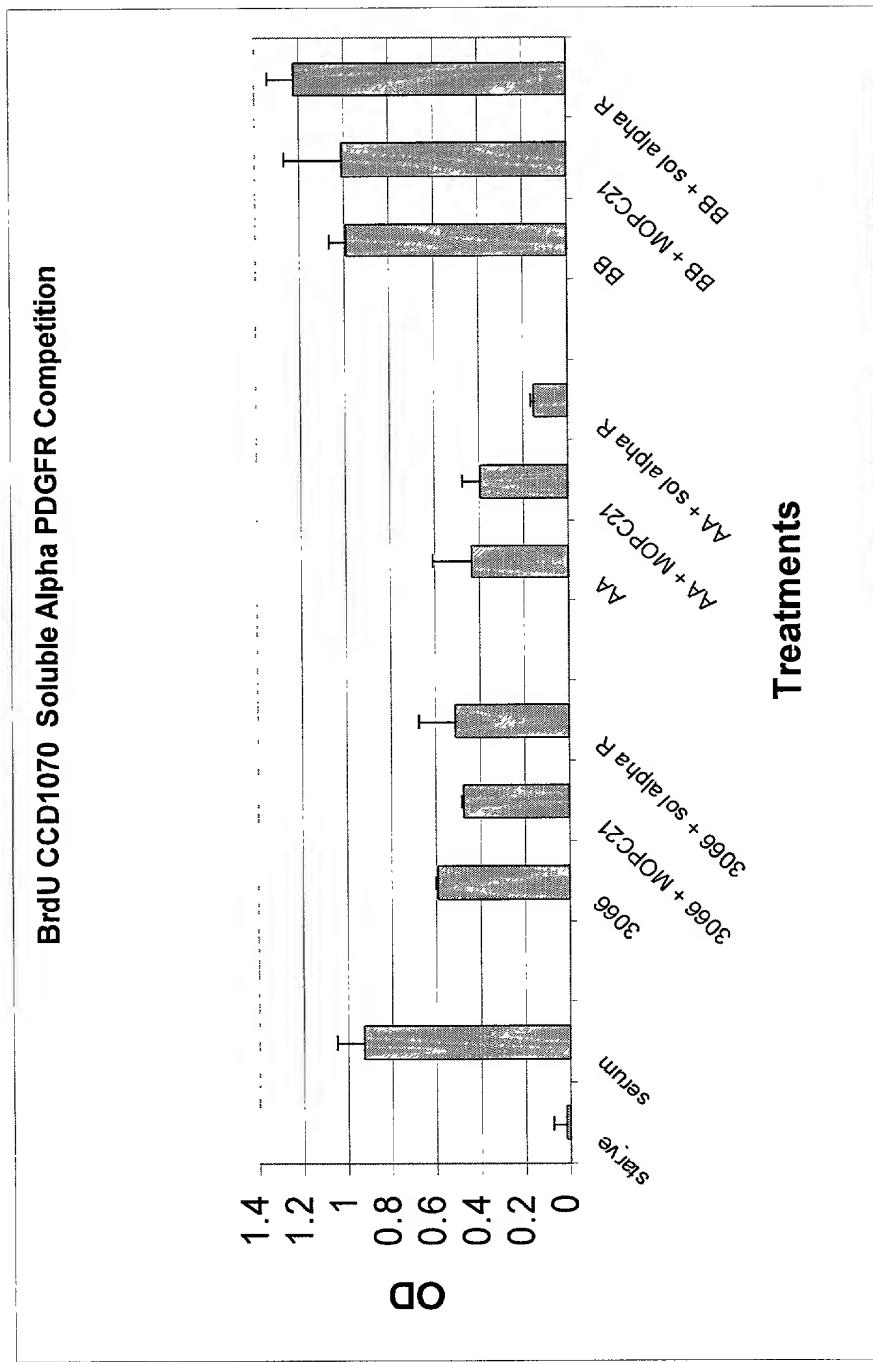
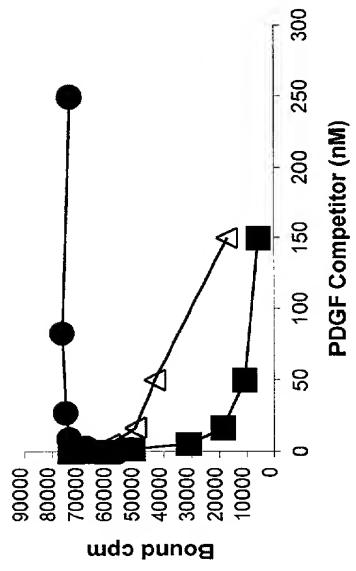


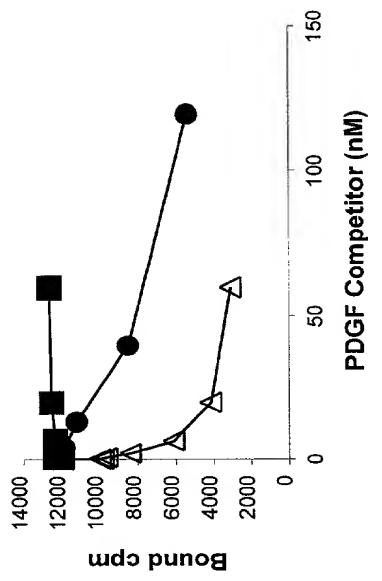
FIG. 26.



**FIG. 27A**



**FIG. 27B**



**FIG. 28**

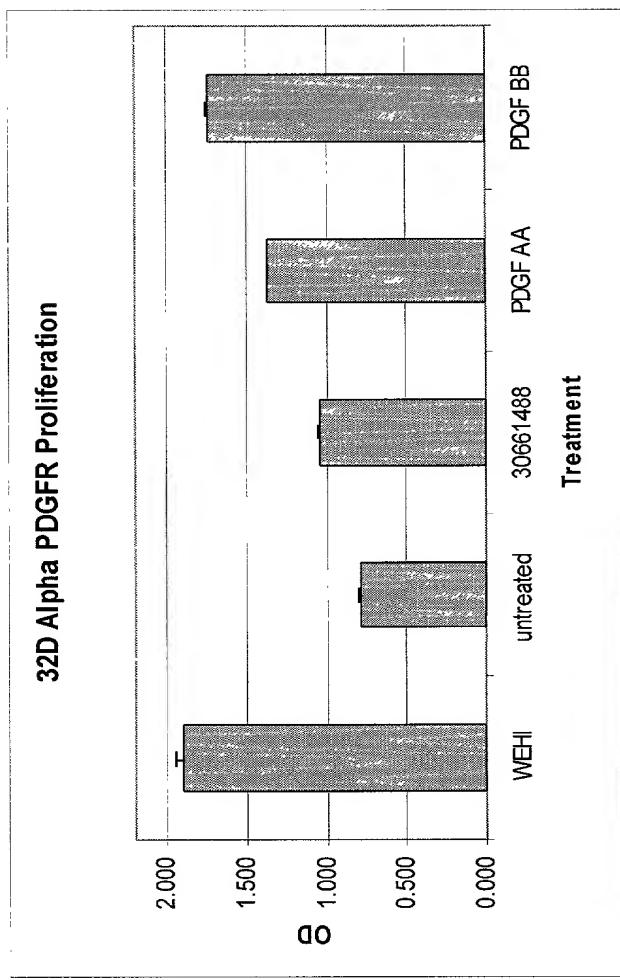


FIG. 29A

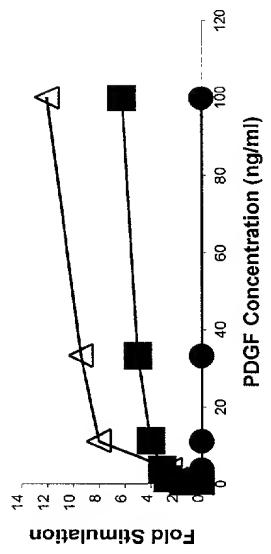


FIG. 29B

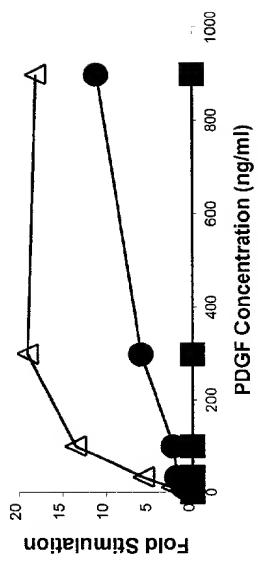


FIG. 29C

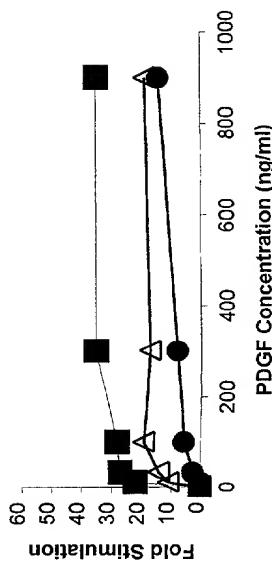


FIG. 29D

